

# Dobrava-Belgrade Virus Spillover Infections, Germany

## Technical Appendix

Table 1. Summary of the serologic and reverse transcription-PCR (RT-PCR) investigations of all serologically and/or RT-PCR-positive *Apodemus* mice\*

Federal state and district	Trapping site	Rodent species (sex)	Rodent no.	DOBV (Slo)-IgG-ELISA†	FRNT‡		Nested RT-PCR L segment	Obtained sequences		
					DOBV-Aa (SK)	DOBV-Af (Slo)		DOBV S segment	DOBV M segment	cyt b (partial)
Lower Saxony Lüneburg	WG	Aa (F)	GER/08/124/Aa	++	<b>80</b>	20	Pos	Partial (nt 1-934); identical to GQ205407	ND	GQ260183
		Aa (M)	GER/08/118/Aa	+++	40	40	Pos	GQ205407 Complete	GQ205412 complete	GQ260182
		Aa (F)	GER/08/125/Aa	+++	ND	ND	pos	Partial (nt 1-934); identical to GQ205407	ND	GQ260184
Mecklenburg-Western Pomerania Demmin	K/A1	Aa (M)	GER/07/1064/Aa	+++	<b>40</b>	20	pos	GQ205404 complete	ND	GQ260176
		Af (M)	GER/07/1058/Af	++	<b>640</b>	80	pos	Partial (nt 219-1675); identical to GQ205404	ND	GQ260175
		Aa (F)	GER/07/1081/Aa	++	ND	ND	pos	ND	ND	GQ260177
		Aa (M)	GER/07/1029/Aa	neg	ND	ND	pos	ND	ND	GQ421162
		Aa (F)	GER/07/1027/Aa	ND	ND	ND	pos	ND	ND	GQ421163
		Af (F)	GER/07/992/Af	neg	ND	ND	pos	ND	ND	GQ421166
		Aa (F)	GER/08/83/Aa	++	<b>80</b>	40	pos	ND	ND	GQ260180
Nordvor-pommern	H	Aa (F)	GER/08/79/Aa	+	ND	ND	pos	ND	ND	GQ260178
		Aa (M)	GER/08/80/Aa	+	ND	ND	pos	ND	ND	GQ260179
		Aa (M)	GER/08/84/Aa	+	ND	ND	pos	ND	ND	GQ260181
		Af (M)	GER/08/131/Af	+	<b>10</b>	<10	pos	GQ205408 complete	GQ205413 complete	GQ260185
		Aa (M)	GER/08/82/Aa	neg	ND	ND	pos	ND	ND	GQ421164
		Af	GER/08/	neg	ND	ND	pos	ND	ND	GQ421165

Güstrow	Pe3	(M) Aa	133/Af GER/07/ 293/Aa	+++	<b>640</b>	80	pos	GQ205401 complete	GQ205409 complete	GQ260171
		(M) Aa	GER/07/ 634/Aa	+	ND	ND	neg	ND	ND	GQ260174
		(F) Aa	GER/07/ 372/Aa	+	ND	ND	neg	ND	ND	GQ260172
	Pe1	(M) Af	GER/07/ 607/Af	++	<10	<10	pos	GQ205402 complete	GQ205410 complete	GQ260186
		(F) Aa	GER/07/ 424/Aa	++	ND	ND	pos	GQ205403 complete	ND	GQ260173
		(M) Aa	GER/05/ 239/Aa	+++	ND	ND	pos	GQ205405 complete	ND	GQ260167
Brandenburg Ostprignitz-Ruppin	To	(M) Aa	GER/06/ 44/Aa	+	ND	ND	neg	ND	ND	GQ260169
		(M) Aa	GER/06/ 49/Aa	+	ND	ND	neg	ND	ND	GQ260170
		(F) Aa	GER/05/ 477/Af	+	ND	ND	pos	GQ205406 complete	GQ205411 complete	GQ260168
	Ka	(M) Af	GER/05/ 477/Af	+	ND	ND	pos	GQ205406 complete	GQ205411 complete	GQ260168
		(M) Aa	GER/05/ 239/Aa	+++	ND	ND	pos	GQ205405 complete	ND	GQ260167

\*FRNT, focus reduction neutralization test; DOBV, *Dobrava-Belgrade virus*; Aa, *Apodemus agrarius*; Af, *A. flavicollis*; Slo, strain Slovenia; SK, strain Slovakia; *cyt b*, *cytochrome b*; ND, not done; nt, nucleotide; neg, negative; pos, positive.

†Optical density values: +++,  $\geq 2.0$ ; ++, 1.9-1.0; +, 0.9-0.2; neg, < lower cut-off (in average 0.041).

‡Endpoint titers.

Table 2. Pairwise nucleotide and amino acid sequence divergence between the entire N- and GPC-encoding DOBV S- and M-segment sequences originating from Germany to those from other regions in Europe\*

Segment and strain	Species	Country (site)	% identity with strain												
			1	2	3	4	5	6	7	8	9	10	11	12	13
S segment ORF															
1. GER/07/293	Aa	GER/Pe3	–	98.5	91.2	98.2	95.1	89.1	87.4	87.2	87.1	87.3	89.0	85.9	91.7
2. GER/07/607	Af	GER/Pe1	99.7	–	91.8	98.0	95.3	88.7	86.9	87.1	87	87.1	89.3	85.7	91.2
3. GER/05/477	Af	GER/Ka	98.8	99.0	–	91.2	91.9	88.9	87.5	86.5	86.8	86.0	89.9	86.7	91.4
4. GER/08/118	Aa	GER/WG	99.3	99.5	98.6	–	94.7	88.8	87.1	87.1	87	87.2	88.6	85.7	91.2
5. GER/08/131	Af	GER/H	99.5	99.7	98.8	99.3	–	89.3	87.4	88	88	88.1	89.6	87.5	91.4
6. SK/Aa	Aa	SVK	98.8	99.0	98.6	98.6	98.8	–	86.4	86.4	85.2	84.6	91.3	86.5	89.4
7. Saa/160V	Aa	EST	96.9	97.2	97.6	96.7	97.4	96.7	–	87.7	87.6	87.4	87.1	84.8	89.7
8. Slo/Af	Af	SVN	97.6	97.9	97.4	97.4	97.6	97.4	96.9	–	96	95.1	87.5	88.2	87.5
9. AP/Af19	Af	GRC	98.3	98.6	98.1	98.1	98.3	98.1	97.2	99.3	–	96.4	87.1	87.6	87.1
10. Esl400/Af	Af	SVK	98.1	98.3	97.9	97.9	98.1	97.9	96.9	99	99.7	–	87.1	87.4	86.6
11. Lipetsk/Aa	Aa	RUS	98.1	98.3	97.9	98.3	98.1	98.8	96.0	96.7	97.4	97.2	–	86.8	89.3
12. Sochi/Ap	Ap	RUS	97.6	97.9	97.4	97.4	98.1	97.4	96.2	97.6	97.9	97.6	96.7	–	86.8
13. Lolland/Aa1403	Aa	DNK	99.3	99.5	99.0	99.0	99.7	99.0	97.6	97.9	98.6	98.3	98.3	98.3	–
M segment ORF															
1. GER/07/293	Aa	GER/Pe3	–	97.9	91.7	97.5	93.2	87.0	86.9	82.8	82.1	82.6	86.7	79.3	–
2. GER/07/607	Af	GER/Pe1	99.1	–	91.9	97.9	93.5	87.4	87.2	83.4	82.4	83.2	87.1	79.5	–
3. GER/05/477	Af	GER/Ka	98.3	98.6	–	92.0	91.7	86.5	87.0	83.3	82.9	83.3	87.2	80.1	–
4. GER/08/118	Aa	GER/WG	98.7	99.2	98.4	–	93.0	86.9	87.4	83.3	82.5	83.0	86.9	79.7	–
5. GER/08/131	Af	GER/H	98.2	98.6	98.8	98.4	–	86.6	87.0	83.1	82.3	83.5	87.3	80	–
6. SK/Aa	Aa	SVK	96.0	96.4	96.2	96.2	96.4	–	87.1	82.5	82.3	82.5	87.6	79.5	–
7. Saa/160V	Aa	EST	95.7	96.0	95.7	95.8	95.9	95.8	–	82.2	82.4	82.1	86.4	79.1	–
8. Slo/Af	Af	SVN	93.6	94.0	94.1	93.8	94.0	93.6	94.1	–	93.7	92.8	83.5	80.4	–
9. AP/Af19	Af	GRC	93.7	94.1	94.2	93.9	94.0	93.6	94.1	98.6	–	93.2	83.2	80.4	–
10. Esl400/Af	Af	SVK	94.0	94.4	94.5	94.1	94.3	94.0	94.3	98.9	99.0	–	83.6	80.8	–
11. Lipetsk/Aa	Aa	RUS	96.7	97.1	96.7	97.0	96.6	97.0	96.2	94.0	94.1	94.4	–	80.6	–
12. Sochi/Ap	Ap	RUS	90.6	91.0	90.9	90.7	90.8	90.5	90.3	93.3	93.3	93.8	91.4	–	–

\*Values above the diagonal are nucleotide sequence differences and values below the diagonal are amino acid differences. ORF, open reading frame.

